E1 cont

SUB F1 cont.

scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, and expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915).--

IN THE CLAIMS:

Please cancel claims 17-20 without prejudice or disclaimer of Applicants' right to pursue the subject matter thereof in a subsequent application.

Please amend claims 1-3, 7, 9 and 10, 11 and 16 as follows (claims 4-6, 8 and 12-15 that have ***not been amended*** are included in this response):

E2

1. (Four times amended) An isolated nucleic acid molecule comprising at least 100 contiguous bases from a rpoB sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 8, 9 and 10

2. (Four times amended) The isolated nucleic acid molecule of claim 1 comprising a rpoB sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 8, 9 and 10.

SUB F2

3. (Four times amended) A probe which is the complement of a rpoB sequence selected from the group consisting of SEQ ID NOS: 2-10.

4. (Thrice Amended) A method of classifying a mycobacteria, comprising providing a sample comprising a mycobacterial rpoB target nucleic acid from a mycobacteria;

E2cont

determining the sequence of a segment of at least 50 contiguous bases from the target nucleic acid;

comparing the determined sequence to at least one sequence selected from the group consisting of SEQ ID NOS: 2-10; and

sub F2 cont.

classifying the mycobacteria from the extent of similarity of the compared sequences.

5. The method of claim 4, wherein at least 100 contiguous bases are determined from the target nucleic acid.

6. (Thrice Amended) The method of claim 4, wherein the determined sequence is compared with at least nine sequences selected from the group consisting SEQ ID NOS: 2-10.

7. (Thrice Amended) A method of classifying a mycobacteria, comprising

providing a sample comprising a mycobacterial rpoB target nucleic acid;

determining the identity of one or more bases in the target sequence at one or more positions corresponding to one or more bases in a sequence selected from the group consisting of SEQ ID NOS: 2-10, wherein the one or more bases of the sequence selected from the group consisting of SEQ ID NOS. 2-10 differ from the corresponding one or more bases in SEQ ID NO. 1 when the sequences are maximally aligned, the identity of the one or more bases characterizing the species of mycobacteria that is present in the sample;

sub F3

comparing the identified one or more bases in the target sequence to at least one sequence selected from the group consisting of SEQ ID NOS: 2-10; and

classifying the mycobacteria from the extent of similarity between the one or more bases identified in the target sequence and the corresponding one or more bases in the compared sequences.

8. (Thrice Amended) The method of claim 7, wherein the identity of at least 10 bases in the target nucleic acid at positions corresponding to the one or more bases in the sequence selected from the group consisting of SEQ ID NOS: 2-10 is determined.

F2 cont.

9. (Four times Amended) The method of claim 8, wherein the identity of at least 20 bases in the target sequence at positions corresponding to the one or more bases in the sequence selected from the group consisting of SEQ ID NOS: 2-10 is determined.

10. (Four times Amended) The method of claim 9, further comprising comparing the at least 20 determined bases with at least 20 bases occupying corresponding positions in each of at least nine sequences selected from the group consisting of SEQ ID NOS: 2-10.

SUB F3 cont.

11. (Four times amended) A sequence-specific polynucleotide probe or primer that hybridizes under stringent hybridization conditions to at least a segment of a mycobacterial rpoB sequence selected from the group consisting of SEQ ID NOS: 2-10 or its complement without hybridizing to the *M. tuberculosis* sequence of SEQ ID NO: 1 or its complement, wherein the segment includes at least about 20 bases of a sequence selected from the group consisting of SEQ ID NOS: 2-10 which differ from the corresponding bases in SEQ ID NO: 1 when the sequences are maximally aligned; wherein said stringent hybridization conditions comprise 5 x SSPE and a temperature of 25-30°C.--

12. (Twice Amended) The sequence-specific polynucleotide of claim 11 that is a probe.

13. (Four Times Amended) The sequence-specific polynucleotide of claim 12, wherein a central position of the probe aligns with the one or more bases of a sequence selected from the group consisting of SEQ ID NOS: 2-10 which differ from the corresponding one or more bases in SEQ ID NO: 1 when the sequences are maximally aligned.

14. (Amended) The sequence-specific polynucleotide of claim 11 that is a primer.

SUB F4

15. (Four Times Amended) The sequence-specific polynucleotide of claim 14, wherein the 3' end of the primer aligns with the one or more bases of a sequence selected